ABSTRACT OF THE DISCLOSURE

The present invention is a method for detecting DNA sequence differences including single nucleotide mutations or polymorphisms, one or more nucleotide insertions, and one or more nucleotide deletions. Labeled heteroduplex PCR fragments containing base mismatches are prepared. Endonuclease cleaves the heteroduplex PCR fragments both at the position containing the variation (one or more mismatched bases) and to a lesser extent, at non-variant (perfectly matched) positions. Ligation of the cleavage products with a DNA ligase corrects non-variant cleavages and thus substantially reduces background. This is then followed by a detection step in which the reaction products are detected, and the position of the sequence variations are determined.